

**Amendments to the Claims**

Please amend Claims 1 and 7-11. Please add new Claims 15-70. The Claim Listing below will replace all prior versions of the claims in the application:

**Claim Listing**

1. (Currently amended) A method of identifying a region of a genome of a cell to which a protein of interest binds, comprising the steps of:
  - a) crosslinking DNA binding protein in the cell to genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA;
  - b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing a mixture comprising DNA fragments to which DNA binding protein is bound;
  - c) removing a DNA fragment to which the protein of interest is bound from the mixture produced in b);
  - d) separating the DNA fragment identified in c) from the protein of interest;
  - e) amplifying the DNA fragment of d);
  - f) combining the DNA fragment of e) with DNA comprising ~~a sequence~~ one or more sequences complementary to one or more intergenic regions of genomic DNA of the cell, under conditions in which hybridization between the DNA fragment and ~~a region of the sequence~~ the one or more sequences complementary to one or more intergenic regions of the genomic DNA occurs; and
  - g) identifying the ~~region of the sequence~~ one or more sequences complementary to the one or more intergenic regions of genomic DNA of f) to which the DNA fragment hybridizes,whereby the region identified in g) is the region of the genome in the cell to which the protein of interest binds.

2. (Original) The method of Claim 1 wherein the cell is a eukaryotic cell.
3. (Original) The method of Claim 1 wherein the protein of interest is selected from the group consisting of: a transcription factor and an oncogene.
4. (Original) The method of Claim 1 wherein the DNA binding protein of the cell is crosslinked to the genome of the cell using formaldehyde.
5. (Original) The method of Claim 1 wherein the DNA fragment of c) to which is bound the protein of interest is identified using an antibody which binds to the protein of interest.
6. (Original) The method of Claim 1 wherein the DNA fragment of e) is amplified using ligation-mediated polymerase chain reaction.
7. (Currently amended) The method of Claim 1 wherein the ~~complement sequence~~ one or more sequences complementary to one or more intergenic regions of the ~~genome~~ genomic DNA of f) is provided on a DNA microarray.
8. (Currently amended) The method of Claim 1 further comprising:
  - h) comparing the ~~region~~ one or more sequences identified in g) with a control.
9. (Currently amended) A method of identifying a region of a genome of a cell to which a protein of interest binds, comprising the steps of:
  - a) formaldehyde crosslinking DNA binding protein in the cell to genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA;

- b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing DNA fragments to which DNA binding protein is bound;
- c) immunoprecipitating the DNA fragment produced in b) to which the protein of interest is bound using an antibody that specifically binds the protein of interest;
- d) separating the DNA fragment identified in c) from the protein of interest;
- e) amplifying the DNA fragment of d) using ligation-mediated polymerase chain reaction;
- f) fluorescently labeling the DNA fragment of e);
- g) combining the labeled DNA fragment of e) with a DNA microarray comprising ~~a sequence~~ one or more sequences complementary to one or more intergenic regions of genomic DNA of the cell, under conditions in which hybridization between the DNA fragment and ~~a region of the sequence~~ the one or more sequences complementary to the one or more intergenic regions of genomic DNA occurs;
- h) identifying the ~~region of the sequence~~ one or more sequences complementary to the one or more intergenic regions of genomic DNA to which the DNA fragment hybridizes by measuring [[the]] fluorescence intensity of the hybridized DNA fragment; and
- i) comparing the fluorescence intensity measured in h) to the fluorescence intensity of a control,

whereby fluorescence intensity in a region of the genome which is greater than the fluorescence intensity of the control in the region indicates the region of the genome in the cell to which the protein of interest binds.

10. (Currently amended) A method of determining a function of a protein of interest which binds to a genome of a cell, comprising the steps of:

- a) crosslinking DNA binding protein in the cell to genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA;
  - b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing a mixture comprising DNA fragments to which DNA binding protein is bound;
  - c) removing the DNA fragment to which the protein of interest is bound from the mixture produced in b);
  - d) separating the DNA fragment identified in c) from the protein of interest;
  - e) amplifying the DNA fragment of d);
  - f) combining the DNA fragment of e) with DNA comprising ~~a sequence~~ one or more sequences complementary to one or more intergenic regions of genomic DNA of the cell, under conditions in which hybridization between the DNA fragment and ~~a region of the sequence~~ the one or more sequences complementary to one or more intergenic regions of the genomic DNA occurs;
  - g) identifying the ~~region of the sequence~~ one or more sequences complementary to the one or more intergenic regions of genomic DNA of f) to which the DNA fragment hybridizes; and
  - h) characterizing the ~~region~~ one or more sequences identified in g),  
wherein the characteristics of the ~~region~~ one or more sequences of h) ~~indicates~~ indicate a function of the protein of interest which binds to the genome of the cell.
11. (Currently amended) A method of determining whether a protein of interest which binds to the genome of a cell functions as a transcription factor, comprising the steps of:
- a) crosslinking DNA binding protein in the cell to the genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA;

- b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing a mixture comprising DNA fragments to which DNA binding protein is bound;
- c) removing the DNA fragment to which the protein of interest is bound from the mixture produced in b);
- d) separating the DNA fragment identified in c) from the protein of interest;
- e) amplifying the DNA fragment of d);
- f) combining the DNA fragment of e) with DNA comprising ~~a sequence~~ one or more sequences complementary to one or more intergenic regions of genomic DNA of the cell, under conditions in which hybridization between the DNA fragment and ~~a region of the sequence~~ the one or more sequences complementary to one or more intergenic regions of the genomic DNA occurs; and
- g) identifying the ~~region of the sequence~~ one or more sequences complementary to the one or more intergenic regions of the genomic DNA of f) to which the DNA fragment hybridizes,

wherein if the ~~region of the sequence~~ one or more sequences complementary to genomic DNA of g) is a regulatory region, then the protein of interest is a transcription factor.

12. (Withdrawn) A method of identifying a set of genes, the members of which are genes for which cell cycle regulator binding correlates with gene expression, comprising:
- (a) identifying a set of genes that is bound in vivo by at least one cell cycle regulator in a selected cell type;
  - (b) comparing the set of genes identified in (a) with genes whose expression levels vary in a periodic manner during the cell cycle of the selected cell type; and
  - (c) identifying genes that are bound by one or more of the cell cycle regulators, thus identifying a set of genes, the members of which are genes whose expression levels vary in a periodic manner during the cell cycle and are bound by at least one

cell cycle regulator, wherein the set identified in (c) is referred to as a set of genes, the members of which are genes for which cell cycle regulator binding correlates with gene expression.

13. (Withdrawn) The method of claim 12, wherein the selected cell type is a yeast cell.
14. (Withdrawn) The method of claim 13, wherein the at least one cell cycle regulator is at least one of the nine known yeast cell cycle transcriptional activators.
15. (New) The method of Claim 1 wherein after the DNA fragment is separated from the protein of interest, the DNA fragment is labeled with a fluorescent dye.
16. (New) The method of Claim 15 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.
17. (New) The method of Claim 1 wherein the DNA fragments are generated using shearing conditions.
18. (New) The method of Claim 1 wherein the one or more intergenic regions of genomic DNA in g) comprises a regulatory region.
19. (New) The method of Claim 18 wherein the regulatory region comprises a promoter region.
20. (New) The method of Claim 19 wherein the promoter region comprises a promoter for two divergently transcribed genes.

21. (New) The method of Claim 1 wherein the one or more intergenic regions of genomic DNA in g) comprises a consensus DNA binding region.
22. (New) The method of Claim 1 wherein the one or more intergenic regions of genomic DNA in g) is a binding site for a transcriptional activator.
23. (New) The method of Claim 1 wherein the one or more intergenic regions of genomic DNA in g) is a binding site for a cell cycle transcription factor.
24. (New) The method of Claim 23 wherein the cell cycle transcription factor regulates one or more genes selected from the group consisting of: G1 genes, G2/M genes, M/G1 genes, G1/S genes and a combination thereof.
25. (New) The method of Claim 9 wherein the cell is a eukaryotic cell.
26. (New) The method of Claim 9 wherein the protein of interest is selected from the group consisting of: a transcription factor and an oncogene.
27. (New) The method of Claim 9 wherein the one or more sequences complementary to one or more intergenic regions of the genomic DNA of g) is provided on a DNA microarray.
28. (New) The method of Claim 9 further comprising:  
j) comparing the one or more sequences identified in h) with a control.
29. (New) The method of Claim 9 wherein after the DNA fragment is separated from the protein of interest, the DNA fragment is labeled with a fluorescent dye.

30. (New) The method of Claim 29 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.
31. (New) The method of Claim 9 wherein the DNA fragments are generated using shearing conditions.
32. (New) The method of Claim 9 wherein the one or more intergenic regions of genomic DNA in h) comprises a regulatory region.
33. (New) The method of Claim 32 wherein the regulatory region comprises a promoter region.
34. (New) The method of Claim 33 wherein the promoter region comprises a promoter for two divergently transcribed genes.
35. (New) The method of Claim 9 wherein the one or more intergenic regions of genomic DNA in h) comprises a consensus DNA binding region.
36. (New) The method of Claim 9 wherein the one or more intergenic regions of genomic DNA in h) is a binding site for a transcriptional activator.
37. (New) The method of Claim 9 wherein the one or more intergenic regions of genomic DNA in h) is a binding site for a cell cycle transcription factor.
38. (New) The method of Claim 37 wherein the cell cycle transcription factor regulates one or more genes selected from the group consisting of: G1 genes, G2/M genes, M/G1 genes, G1/S genes and a combination thereof.



39. (New) The method of Claim 10 wherein the cell is a eukaryotic cell.
40. (New) The method of Claim 10 wherein the protein of interest is selected from the group consisting of: a transcription factor and an oncogene.
41. (New) The method of Claim 10 wherein the DNA binding protein of the cell is crosslinked to the genome of the cell using formaldehyde.
42. (New) The method of Claim 10 wherein the DNA fragment of c) to which is bound the protein of interest is identified using an antibody which binds to the protein of interest.
43. (New) The method of Claim 10 wherein the DNA fragment of e) is amplified using ligation-mediated polymerase chain reaction.
44. (New) The method of Claim 10 wherein the one or more sequences complementary to one or more intergenic regions of the genomic DNA of f) is a DNA microarray.
45. (New) The method of Claim 10 further comprising:
  - i) comparing the region identified in g) with a control.
46. (New) The method of Claim 10 wherein after the DNA fragment is separated from the protein of interest, the DNA fragment is labeled with a fluorescent dye.
47. (New) The method of Claim 46 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.

48. (New) The method of Claim 10 wherein the DNA fragments are generated using shearing conditions.
49. (New) The method of Claim 10 wherein the one or more intergenic regions of genomic DNA in g) comprises a regulatory region.
50. (New) The method of Claim 49 wherein the regulatory region comprises a promoter region.
51. (New) The method of Claim 50 wherein the promoter region comprises a promoter for two divergently transcribed genes.
52. (New) The method of Claim 10 wherein the one or more intergenic regions of genomic DNA in g) comprises a consensus DNA binding region.
53. (New) The method of Claim 10 wherein the one or more intergenic regions of genomic DNA in g) is a binding site for a transcriptional activator.
54. (New) The method of Claim 10 wherein the one or more intergenic regions of genomic DNA in g) is a binding site for a cell cycle transcription factor.
55. (New) The method of Claim 54 wherein the cell cycle transcription factor regulates one or more genes selected from the group consisting of: G1 genes, G2/M genes, M/G1 genes, G1/S genes and a combination thereof.
56. (New) The method of Claim 11 wherein the cell is a eukaryotic cell.

57. (New) The method of Claim 11 wherein the DNA binding protein of the cell is crosslinked to the genome of the cell using formaldehyde.
58. (New) The method of Claim 11 wherein the DNA fragment of c) to which is bound the protein of interest is identified using an antibody which binds to the protein of interest.
59. (New) The method of Claim 11 wherein the DNA fragment of e) is amplified using ligation-mediated polymerase chain reaction.
60. (New) The method of Claim 11 wherein the one or more sequences complementary to one or more intergenic regions of the genomic DNA of f) is provided on a DNA microarray.
61. (New) The method of Claim 11 further comprising:  
h) comparing the region identified in g) with a control.
62. (New) The method of Claim 11 wherein after the DNA fragment is separated from the protein of interest, the DNA fragment is labeled with a fluorescent dye.
63. (New) The method of Claim 62 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.
64. (New) The method of Claim 11 wherein the DNA fragments are generated using shearing conditions.
65. (New) The method of Claim 11 wherein the regulatory region comprises a promoter region.

66. (New) The method of Claim 65 wherein the promoter region comprises a promoter for two divergently transcribed genes.
67. (New) The method of Claim 11 wherein the one or more intergenic regions of genomic DNA in g) comprises a consensus DNA binding region.
68. (New) The method of Claim 11 wherein the one or more intergenic regions of genomic DNA in g) is a binding site for a transcriptional activator.
69. (New) The method of Claim 11 wherein the one or more intergenic regions of genomic DNA in g) is a binding site for a cell cycle transcription factor.
70. (New) The method of Claim 69 wherein the cell cycle transcription factor regulates one or more genes selected from the group consisting of: G1 genes, G2/M genes, M/G1 genes, G1/S genes and a combination thereof.